(5') 1	SDLEQERRAKEKLQEQQ
18	SDLEQDRLAKEKLQEQQ
35	SDLEQERLAKEKLQEQQ
52	SDLEQERRAKEKLQEQQ
69	SDLEQERRAKEKLQEQQ
86	SDLEQDRLAKEKLQEQQ
103	SDLEQERRAKEKLQEQQ
120	SDLEQERRAKEKLQEQQ
137	SDLEQERLAKEKLQEQQ
154	SDLEQERRAKEKLQEQQ
171	SDLEQERRAKEKLQEQQ
188	SDLEQERRAKEKLQEQQ
205	RDLEQ
210	RKADTKKNLERKKEHGDILAEDLYGRLEIP
240	AIELPSENERGYYIPHQSSLPQDNRGNSRD
270	SKEISIIEKTNRESITTNVEGRRDIHKGHL
300	EEKKDGSTKPEOKEDKS 316 (3')

AAAGCGATCTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC **AAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAGTTACAAGAGCAGC** AAAGCGATTTAGAACAAGAGACTTGCTAAAGAAAGTTGCAAGAACAAC AAAGCGATCTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC AAAGCGATTTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC AAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAGTTACAAGAGCAGC AAAGCGATTTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC AAAGCGATTTAGAACAAGAGACTTGCTAAAGAAAAGTTGCAAGAACAAC AAAGCGATTTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC **AAAGCGATTTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAGCAGC** AAAGCGATTTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC AAAGCGATTTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC **AAAGAGATTTAGAACAA** 205 256 358 409 460 307 613 511 562

FIGURE 2

AAAACAAATAGAGAATCTATTACAACAAATGTİGAAGGACGAAGGGATATA

CATAAAGGACATCTTGAAGAAAAAAAGATGGTTCAATAAAACCAGAACAA

AAAGAAGATAAATCT

CAGGACAACAGAGGAATAGTAGAGATTCCAAGGAAATATCTATAATAGAA

ATATTAGCAGAGGATTTATATGGTCGTTTAGAAATACCAGCTATAGAACT1 CCATCAGAAAATGAACGTGGATATTATATACCACATCAATCTTCTTTACC1

AGGAAGGCTGATACGAAAAAAATTTAGAAAGAAAAAAGGAACATGGAGA1

630

681 732 783 RDELFNELLNSVDVNGEVKENILEESQVNDDIFNSLVJSVQQEQQ HNVEEKVEESVEENDEESVEENVEENVEENDDGSVASSVEESI ASSVDESIDSSIEENVAPTVEEIVAPTVEEIVAPSVVEKCAPSVE ESVAPSVEESVAEMLKER

NSRDSKEISIIEKTNRESITTNVEGRRDIHK

LSA-TER

DELFNELLNSVDVNGEVKENILEESQ LEESQVNDDIFSNSLVKSVQQEQQHNV VEKCAPSVEESVAPSVEESVAEMLKER

7295-NRI 7295-NRII 7295-Rep

NUCLEOTIDE SEQUENCE OF THE LSA GENE 5' END

(NON-CODING 5' END)

1 AAAGTATACATCTTCCTTCTTTACTTCTTAAA

(CODING 5' END, UNIQUE)

- 33 ATGAAACATATTTTGTACATATCATTTTACTTTATCCTTGTTAATTTATTG
- 84 ATATTTCATATAAATGGAAAGATAATAAAGAATTCTGAAAAAGATGAAATCA
- 135 TAAAATCTAACTTGAGAAGTGGTTCTTCAAATTCTAGGAATCGAATAAATGA
- 186 GGAAAATCACGAGAAGAAACACGTTTTATCTCATAATTCATATGAGAAAACT
- 237 AAAAATAATGAAAATAATAAATTTTTCGATAAGGATAAAGAGTTAACGATGT
- 288 CTAATGTAAAAAATGTGTCACAAACAAATTTCAAAAGTCTTTTAAGAAATCT

- 441 AAGGGCAAGACGAAAACAGACAAGAAGATCTTGAAGAAAAAGCA

(CODING 5' END, repetitive)

- 492 GCTAAAGAAAGTTACAGGGGCAACAAGCGATTCAGAACAAGAGAGACGT
- 543 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGAC<u>T</u>T
- 645 GCTAAAGAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGAGAGAC<u>T</u>T
- 696 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
- 747 GCTAAAGAAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACGT
- 798 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGAC<u>T</u>T
- 849 GCTAAAGAAAAGTT<u>A</u>CAAGA<u>G</u>CA<u>AGAAGGGATTTAGAACAAGAT</u>AGAC<u>T</u>T
- 951 GCTAAAGAAAGGTTGCAAGAACAACAAAGCGATTTAGA 988

LSA.5'/ATG - -> 1-phase Translation

sequence 956 b.p. ATGAAACATATT ... AAGCGATTTAGA linear DNA

CAT his arg AAG lys GAA glu CTT val AAA AGT lys ser GAT asp CAC his TTT phe TTG len AAG 1ys ATA ile AAA 1ys TTC phe AAT asn AAC asn TG TAC ATA TCA TTT TAC TTT ATC CTT GTT AAT TTA TTG ATA eu tyr ile ser phe tyr phe ile leu val asn leu leu ile 91 / 31

TA ATA AAG AAT TCT GAA AAA GAT GAA ATC ATA AAA TCT AAC le ile lys asn ser glu lys asp glu ile ile lys ser asn 151 / 51

AAT TCT AGG AAT CGA ATA AAT GAG GAA AAT CAC GAG AAG AAA ISN ser arg asn arg ile asn glu glu asn his glu lys lys can ser arg ash arg ile asn glu glu asn his glu lys lys can tyr glu lys thr lys asn asn glu asn asn lys phe phe ser tyr glu lys thr lys asn asn glu asn asn lys phe phe TTC phe TTA GAA AAT AAA ' CAA ACA AAT ' TCA AAA lys AAT GTG asn val CTT , TTC . AAA lys 111 ATA ile GTA val / AAT asn asn 331 GAG glu lys 271 AAT AAT TCT AGG A asn ser arg a TCT TCA ATG met GTT / 1 / AAA CAT ATT TTG T/ / lvs his ile leu t ATA TCA ACG thr GGT gly AAT GGA AAG A asn gly lys i / 41 GGT TCT TCA A TCA ser CAT AAT his asn 81 GAG TTA glu leu 101 AAT CTT CTT ser 61 TCT 1 ATG 61 61 ATA 121 121 181 174 GAT asp 301

FIGURE 7A

	999	8	, ס	999	۸۱۵		AGC	Ser		GAA	11 2	S D	AGA	arg		AAA	l V S		TTG	leu	i)
	AAA	lvs		CAG	מן	; 0	CAA	gln	.	TTA	Jeu	; ;	GAG	glu	;)	GCT	ala		AAG	lvs	
	ATT	ile		TTA	le II	3	CAA	gln)	GAT	asp	<u>.</u>	SA	gln)	CGT	arg)	GAA	glu	.
	TAT	tvr	,	AAG	1 1 5		GAA	glu)	AGC	Ser	i	GAA	glu)	AGA	arg)	AAA	lvs	•
	AAA	lvs	•	GAA	glu	0	CAA	gln)	CAA	gln	; 5	TTA	leu		GAG	glu)	GCT	ala	
	AAA	lvs	•	AAA	1 1 5		TTG	leu		CAA	gln	;)	GAT	asp	-	Y Y	gln)	CGT	arg)
	AAA	lys	· .	GCT	ala		AAG	lys	•	GAA	glu	.	AGC	ser		GAA	glu)	AGA	arg)
	GAT	asp	•	SCA GCA	ala		GAA	glu	,	CAA	gln)	CAA	gln)	TTA	leu		GAG	glu)
	GAC	asp	•	AAA	lvs	•	AAA	lys	•	TTG	leu		CAA	gln)	GAT	asp	•	CAA	gln	•
	.GAT	asp	•	GAA	glu)	GCT	ala		AAG	lys		GAA	glu)	AGC	ser		GAA	glu	,
131	GAT	asp	151	GAA	glu	171	CGT	arg	191	GAA	glu	211	CAA	gln	231	CAA	gln	$\overline{2}51$	TTA	len	
\	AAT	asn	\	CTT	leu	\	AGA	arg	_	AAA	lys	· ~	TTG	len	_	CAA	gln	_	GAT	asp	
391	ATA	ile	451	GAT	asp	$51\dot{1}$	GAG	glu	571	GCT	ala	631	AAG	lys	691	GAA	glu	751	AGC	ser	
	ATA	ile		GAA	glu)	CAN	gln		CTT	len		GAA	nlg	ı	CAA	gln		CAA	gln	,
	CAC	his		CAA	gln)	GAA	glu		AGA	arg)	AAA	lys	ı	TTG	len		CAA	gln	
	GAA	glu		AGA	arg)	TCA	Ser		GAG	glu		GCT	ala		AAG	lys		GAA	glu	
	ATT	ije		AAC	asn		GAT	asb		CAA	gln		CGT	arg	_	GAA	glu		CAA	gln	
•													AGA			-			-		
_	AAA	lys	\	GAC	asp	\	CAA	gln	\	TTA	len	\	GAG	glu	_	CCT	ala	\	. AAG	lys	
361	999	gly	421	CAA	gln	481	CAA	gln	541	GAT	asb	601	CAA	gln	661	CTT	len	721	GAA	g.Jn	

FIGURE 7B

CAG gln GAT GAG glu AGC ser CAA gln CAA gln TTA leu TTA CAA gln GAT asp AAG lys GAA glu AGC ser GAA glu CAA gln CAA gln AAA lys TTG CAA gln GCT ala AAG lys GAA glu AGA CTT arg leu AAA GAA lys glu CAA gln TTG leu 271 GAG glu 291 GCT ala 311 AGG CAA CAA CTT CTT leu / GAA 811 GAA GAA 871 AGA 931 1ys TTA leu GAT asp GCT GAT asp CAA gln AGA CGT arg arg AGC ser GAA GAA CAA gln TTA leu GAG glu 261 CAA gln 281 281 6AT 301 CAA GAA GAA glu / AGC Ser / GAA glu 781 CAA gln 841 CAA gln 901 TTA

FIGURE 7C

NUCLEOTIDE SEQUENCE OF THE LSA GENE 3' END

(CODING 3' END, REPETITIVE)

- 1 CAAGAACAACGAGCGATCTAGAACAAGAGAGACGT
- 37 GCTAAAGAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGATAGACTT
- 88 GCTAAAGAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAGACTT
- 139 GCTAAGAAAGTTGCAAGAACAACAAAGCGATCTAGAACAAGAGAGACGT
- 190 GCTAAAGAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
- 241 GCTAAAGAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGATAGACTT
- 292 GCTAAAGAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAGACGT
- 343 GCTAAAGAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACGT
- 394 GCTAAGAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT
- 445 GCTAAAGAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
- 496 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
- 547 GCTAAGAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
- 598 GCTAAAGAAAGTTGCAAGAGCAGCAAAGAGATTTAGAACAA

(CODING 3' END, UNIQUE)

- 640 AGGAAGGCTGATACGAAAAAAATTTAGAAAGAAAAAAGGAACATGGAGAT
- 691 ATATTAGCAGAGGATTTATATGGTCGTTTAGAAATACCAGCTATAGAACTT
- 742 CCATCAGAAAATGAACGTGGATATTATATACCACATCAATCTTCTTTACCT
- 793 CAGGACAACAGAGGAATATAGAAGAATTCCAAGGAAATATCTATAATAGAA
- 844 AAAACAAATAGAGAATCTATTACAACAAATGTTGAAGGACGAAGGGGATATA
- 895 CATAAAGGACATCTTGAAGAAAAGAAAGATGGTTCAATAAAACCAGAACAA 946 AAAGAAGATAAATCTGCTGACATACAAAATCATACATTAGAGACAGTAAAT
- 997 ATTTCTGATGTTAATGATTTTCAAATAAGTAAGTATGAGGATGAAATAAGT
- 1048 GCTGAATATGACGATTCATTAATAGATGAAGAAGAAGATGATGAAGACT
- 1099 TAGACGAATTTAAGCCTATTGTGCAATATGACAATTTCCAAGATGAAGAAA
- 1150 ACATAGGAATTTATAAAGAACTAGAAGATTTGATAGAGAAAAATGAAAATT
- 1201 TAGATGATTAGATGAAGGAATAGAAAAATCATCAGAAGAATTATCTGAAG
- 1252 AAAAAATAAAAAAGGAAAGAAATATGAAAAAACAAAGGATAATAATTTTA
- 1303 AACCAAATGATAAAAGTTTGTATGATGAGCATATTAAAAAATATAAAAATG
- 1354 ATAAGCAGGTTAATAAGGAAAAGGAAAAATTCATAAAATCATTGTTTCATA
- 1405 TATTTGACGGAGACAATGAAATTTTACAGATCGTGGATGAGTTATCTGAAG
- 1456 ATATAACTAAATATTTTATGAAACTA<u>TAA</u> (stop)

(NON-CODING 3' END)

1485 AAGGTTATATATTT 1498

LSA.3'.ALL -> 1-phase Translation

CAAGAACAACAA ... GGTTATATTT 1496 b.p. DNA sequence

CAA glñ GAA glu CAA GAT asp CAA CGT AAA lys GAA glu GAA TTG AGC Ser nlg AGA arg leu CAA gln GCT ala CTA CAA gln GAG glu AAG len lys TTG leu CAG gln asb CAA gln GAA glu GAT CTT GAA AAG glu lys GAT AGA asp arg GAG glu GAA glu AAA AGC ser lys GCT CAA gln CAA TTA GAT asp AAA lys TTA CAA gln CAA CGT arg GCT ala AAG lys GAA glu GAA glu AGC ser AGA GAA glu CAA gln TTA CGT arg CAA gln GAG glu AGA arg AAA GAT TTG leu CAA gln CAA gln GAG GCT ala AAG lys AGC ser GAA glu GAA GAA CAA (glu glu glu gl / 31 AGA CTT (arg leu a GAA glu 71 CAA gln CAA CAA 1111 TTA AAA CAA gln / lys TTG 31 CTA leu 91 GAT asp 151 6CT 211 211 271 6AA 6AA 81u 331 asp GAT CAA gln GAA glu SA CAA CTT gln CAA AGC gln ser GAA glu AGA arg AAA lys **TTG** len GAG glu TTA GCT ala AAG lys GAG glu 1 / 1 CAA GAA CAA C gln glu gln g 61 / 21 CAA AGC GAT 1 gln ser asp 1 121 / 41 TTA GAA CAA G leu glu gln g 181 / 61 GAG AGA CGT G glu arg arg a 241 / 81 CGT arg 81 81 GAA GAA 6101 CAA 81n 81n ser GAA GAA AGA arg / AAA lys

FIGURE 9A

TTA leu GAG glu AAA 1ys TTA CAA gln ATA ile CAA gln GAT asp CAA gln CGT arg AAA lys CAT his ATA ile CGT arg GAA glu AGA arg ACG thr AGC ser GAA glu GGT gly CCA pro TCT CAA gln TTA GAG glu GAT asp CAA gln ATA ile ATA ile TAT tyr TTG leu GAT asp CAA gln GAA glu CAA gln GCT ala TTA TAT tyr AAG lys AGC ser GAA glu GAA glu AAG lys GAT asp TAT AAG lys AGG arg GAA glu TCC CAA gln CAA gln TTA GGA glý GAG glu GAT asp AAA 1ys TTG leu CAA gln CAA gln CGT GAT asp GCA ala GCT ala AGA arg AAG 1ys GAA glu AGC ser GAA glu TTA GAA glu CGT arg GAA glu AAT asn AGT ser CAA gln CAA gln TTA leu ATA ile AGA arg GAA glu AAT asn GAT asp AAA 1ys TTG leu CAA gln GAT asp CAA glu leu leu CAA CAA CAA CAA CAA CAA CAA AGA asn TTA GCT ala GAG glu AAG lys GAG glu AAG lys GAA glu GAC asp GAA glu CAA gln CAA gln GAT asp CGT arg AAA 1ys ATA ile CAG gln AAA lys TTG AGC ser GAA glu AGA arg AGA arg / 121
CAA CAA
gln gln gln
A 141
GAT TTA
asp leu
/181
CGT GCT
arg ala
/181
GAA AAG
glu lys
/ 201
TTA GAA
leu glu
/ 241
ATA CCA
ile pro
/ 261
TCT TTA
ser leu

FIGURE 9B

TCT ser gln GAA glu GAT asp TTA S AAA lys CAT his AAA 1ys GAA glu CAA gln asn phe 111 AAT ATA ile GAT asp GAT asp GAT GAA TTC phe AAA lys glu GAT GAA glu ATA ile AAT asn AAT asn AAT asn GAA glu AGG arg AAA 1ys TTA GAC asp GTT AAA lys val GAA glu CAA gln CGA arg TCA ser GAT asp TAT GAG glu TCT ser GGA gly GAA glu TCT GAT asp CAA gln ATA ile TTA GAA CCA pro ile GAC asp GTG val ATT TTG len GAA glu AAA 1ys AAT GAT asp GTT val ATT ile TAT GAA glu AAT asn ATA ile GTA val CCT GAA glu GAA glu TCA ser 291 ACA ACA / thr thr ; 311 GGT TCA / gly ser 331 GAG ACA (glu thr) 351 ser ala 371 TTT AAG AAA TCA lys ser phe lys 391 glu leu 411 GAA CTA tyr lys 1231 / ATA GAA ile glu AAA GAA leu glü thr 1 1051 GAA / glu i 1111 GAC (TAT , 871 TCT ser 931 AAA 1ys 991 GAA glu AAG 1ys CAT his GAT asp TTA ATT ile leu GGA gly GAA glu AGA arg AAT asn asp GAG glu GAC GGA gly GAA ATA CAA ile gln 341 AAG TAT lys tyr 361 asp glu 381 AAC ATA asn ile asn GAA GAT asp glu GAT GAA 841 / GAA AAA glu lys 901 / GGA CAT gly his 961 / GCT GAC ala asp 1021 / ATA AGT ile ser 1081 / GAA GAT GAA

FIGURE 9C

ser leu GAA AAA glu lys GAT asp GTG val CCA AAT GAT AAA AGT pro asn asp lys ser GAA glu AAA 1ys phe ATA ATT ile TAT tyr GAT len AAG AAA 1 1ys 1ys 1 441 GAG CAT / glu his 1 461 AAA TCA 1 1ys ser 1 TCT GAA lys gly 1 1321 / TAT GAT G tyr asp g 1381 / TTC ATA A phe ile 1 1441 / GAG TTA 7

FIGURE 9D

LSN.3'STOP -> 1-phase Translation

1482 b.p. CAAGAACAACAA ... ATGAAACTATAA linear DNA sequence

asp GAA glu CAA gln GAG AGA glu arg GAA glu AAA lys: TTG AGC ser AAG 1 CAA gln CAA gln CTA leu GCT GAA , TTG leu GAT asp CAA gln CAG gln CTT CAA GAT AGA (gln asp arg [·] GCT AAA (ala lys { TTA GAA leu glu AAG lys CAA AGC gln ser GAG glu glu GAA glu CAA gln GAG AGA CGT (gluargarga AAA lys CAA gln TTA asp GAT GAA AAG glu lys GCT ala GAA glu GÄA glu AGC ser AGA CGT arg TTG CAA leu gln CAA gln TTA GAT AAA 1ys CAA gln CAA gln GAG glu GCT ala AAG lys GAA glu GAA glu AGC ser 31 CTA leu 91 GAT asp 151 lys 271 GAA ala 211 AAG glu 33:1 AGC ser GAT asp CÁA gln CTT GAÀ glu CAA gln CAA gln / 1 1 GAA CAA CAA AGC G n glu gln ger ? GAA glu AGA arg AAA 1ys CAG gln TTG leu TTA GAG glu GCT ala AAG 1ys GAG glu asp | 41 CAA (CAA (61 61 CGT (arg ; 81 6AA , CAA (AGC GAT GAA glu / ser AGA arg / AAA lys

FIGURE 10A

CAA gln TTA GAG glu TTA leu AAA lys ATA ile CAA gln CGT arg GAT asp CGT arg AAA lys CAT his AGA arg GGT CCA pro TCT ACG thr GAA glu AGC ser GAA glu TTA GAG glu CAA gln CAA gln GAT ATA ile ATA ile TAT CAA gln CAA gln TTA leu TAT GAA glu TTG leu GAT asp GCT ala GAT asp TAT tyr AGC ser AAG 1ys AAG lys GAA glu GAA glu AAG 1ys CAA gln TTA leu GAA glu CAA gln AGG arg GAG glu GGA gly TCC AAA lys TTG leu CAA gln GAT CAA gln . GAT asp GCA ala CGT arg ATA TTA ile leu GCT GAA glu AGA arg AAG 1ys GAA glu GAA glu AGC ser CGT arg GAA glu CAA gln CAA gln TTA leu AAT asn AGT ser GAT AGA TTG leu CAA gln GAT GAA glu AAT asn AAA 1ys GAA glu CAA CCAA CCAT his CCA CAA CAA gln / CTT leu AGA arg GAA glu GAC asp GAG glu AAG lys GAG glu AAG lys TTA GAA glu AAA lys asp ATA ile CGT arg CAA gln CAA gln GAT CAG gln AGA arg AGA arg GCT ala AAA lys TTG AGC ser GAA glu CCT 121 CAA CAA Beln 161 161 161 161 161 174 174 CCA CCA 160

FIGURE 10B

GAA glu TTA CAA gln GAT asp AAA 1ys TTG leu TCT ser CAA gln AAT asn ATA ile AGT ser CAT his AAA 1ys phe GAA glu GAT AAA asp lys GAA glu ATA ile GAT asp AAA 1ys asp GAT asp TTC phe **GAT** GAT asp. AAT GAA glu GAA glu asn ATA ile AAT asn AAT TAT GAC tyr asp. CCA AAT (AAA lys TTA AGG arg GAA glu AAA 1ys GTT val GAT GAG glu CAA gln TCA ser CGA arg TCT ser AAA lys CAA gln ATA ile GGA gly GAA GAT asp TCT ser TTA GAA glu CCA pro GAC GAA glu TTT phe ATT ile GTG val TTG AAT asn GAA glu AAT GTT asn val AAA 1ys GAT asp AAG GAT AAT AAT lys asp asn asn TAT tyr ATT ile AAA TCA TCA G lys ser ser g 431 GAA glu GTA ATA ile CCT GAA glu gly ser 331 GAG ACA (glu thr 351 AGT GCT (ser ala 8 371 TTT AAG (phe lys p GAA CTA glu leu 411 291 ACA ACA thr thr 311 GGT TCA TCA Ser lys asp 991 / ACA TTA C thr leu E 1051 / GAA ATA A glu ile s asp glu F 1171 / TAT AAA (tyr lys E 1231 / ATA GAA / ile glu l GAC GAA GAT 871 TCT / ser · 931 AAA (GAA glu GAT asp ATT ile GGA gly GAA glu AAG lys CAT his TTA leu GAA GAC asp GGA gly AAT asn GAG glu GAA. glu TAT leu glu 321 ATA CAA ile gln 341 AAG TAT lys tyr 361 GAT GAA asp glu 381 AAC ATA asn ile 281 ACA AAT thr asn AAG AAA lys lys TTA GAT leu asp 421 glu 301 CTT GCT GAC ala asp 1021 / ATA AGT ile ser 1081 / GAA GAT glu asp 1141 / GAA GAA

FIGURE 10C

GTT AAT AAG GAA AAG GAA AAA val asn lys glu lys glu lys GAT asp TTA CAG ATC GTG leu gln ile val AA AAA TAT AAA AAT GAT AAG CAG GTT AAT AAG GAA AAG GA/ys lys tyr lys asn asp lys gln val asn lys glu lys gli 1411 / 471

TT CAT ATA TTT GAC GGA GAC AAT GAA ATT TTA CAG ATC GT(he his ile phe asp gly asp asn glu ile leu gln ile variata ACT AAA TAT TTT ATG AAA CTA TAA AAG GTT ATA TAT Ile the lys tyr phe met lys leu AAA lys ATA ile TTT phe 1321 / 441
TAT GAT GAG CAT ATT A/
tyr asp glu his ile ly
1381 / 461
TTC ATA AAA TCA TTG T
phe ile lys ser leu pl
1441 / 481
GAG TTA TCT GAA GAT A'
glu leu ser glu asp i

FIGURE 10D